

# Bacterial activity and community composition response to the size-reactivity of dissolved organic matter

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Heterotrophic bacteria respond dynamically to variations in organic matter availability in the dark ocean. However, our knowledge on how the differences in sized and/or reactivity of dissolved organic matter (DOM) affect the bacterial community dynamics is still scarce. Our study aims to investigate the response of bacterial activity and community composition to the degradability of filtered and of size-fractionated DOM. A natural bacterial community isolated from Mediterranean Water (MW; at 1000 m depth) was inoculated in seawater from the same location subjected to three different treatments: 0.2µm-filtered seawater (control), low molecular weight fraction (LMW) obtained by ultrafiltration, and the combination of low and high molecular weight fractions at the original ratio (H+L). Bacterial abundance and activity was monitored every 24h over 6 days, while bacterial community composition and DOM characterization were assessed at the beginning (day 0), middle (day 4) and at the end of the experiment (day 6). Low (LNA) and high nucleic acid content (HNA) bacterial abundance, as well as leucine incorporation rates, were consistently higher in the H+L incubations than in the LMW treatments, indicating different reactivity of the two organic matter size fractions. Moreover, actively respiring cells, estimated as CTC-positive cells, highly correlated to humic-like substances (FDOM-M;  $R=0.7$ ,  $P<0.05$ ,  $n=9$ , Spearman Rank Order), particularly in the H+L incubations. Interestingly, LNA cell abundance was highly correlated with the slope ratio (SR) values ( $R=-0.8$ ,  $P<0.05$ ,  $n=9$ , Spearman Rank Order), indicating that bacteria belonging to the LNA population are tightly linked to the molecular weight or aromaticity of the DOM. Taken together, our results indicate differences in the bio-reactivity of the low and high molecular weight size classes of DOM associated to the phylogenetic composition of the bacterial communities.

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